

1 2. (Amended) The nucleic acid of claim 1 comprising a complete rpoB  
2 sequence [shown in Table 1] designated as any of the SEQ ID NOS: 1-181.

1 3. (Amended) A set of probes perfectly complementary to and spanning a  
2 full-length sequence [shown in Table 1] designated as of the SEQ ID NOS: 1-181.

1 4. (Amended) A method of classifying a mycobacteria, comprising  
2 providing a sample comprising a mycobacterial rpoB target nucleic acid from a  
3 mycobacteria;

4 determining the sequence of a segment of at least 50 contiguous bases from the  
5 target nucleic acid;

6 comparing the determined sequence to at least one sequence [shown in Table 1]  
7 designated as SEQ ID NOS: 1-181;

8 classifying the mycobacteria from the extent of similarity of the compared  
9 sequences.

1 5. (As Filed) The method of claim 4, wherein at least 100 contiguous  
2 bases are determined from the target nucleic acid

1 6. (Amended) The method of claim 4, wherein the determined sequence is  
2 compared with at least ten sequences [shown in Table 1] designated as SEQ ID NOS: 1-181.

1 7. (Amended) A method of classifying a mycobacteria, comprising  
2 providing a sample comprising a mycobacterial rpoB target nucleic acid;  
3 determining the identity of one or more bases in the target sequence at one or  
4 more positions corresponding to one or more of the highlighted positions in a sequence [shown  
5 in Table 1] designated as any of the SEQ ID NOS: 1-181, the identity of the one or more bases  
6 characterizing the species of mycobacteria that is present in the sample.

1 8. (Amended) The method of claim 7, wherein the identity of at least 10  
2 bases in the target nucleic acid at positions corresponding to highlighted positions in a  
3 sequence [shown in Table 1] designated as any of the SEQ ID NOS: 1-181 is determined.

1 9. (Amended) The method of claim 8, wherein the identity of at least 20  
2 bases in the target sequence at highlighted positions [shown in Table 1] designated as any of  
3 the SEQ ID NOS: 1-181 are identified.

1 10. (Amended) The method of claim 9, further comprising comparing the  
2 20 determined bases with 20 bases occupying corresponding positions in each of at least ten  
3 sequences [from Table 1] designated as any of the SEQ ID NOS: 1-181.

1 11. (Amended) A sequence-specific polynucleotide probe or primer that  
2 hybridizes to a segment of a mycobacterial rpoB sequence [shown in Table 1] designated as  
3 any of the SEQ ID NOS: 1-181 or its complement without hybridizing to the M. tuberculosis  
4 sequence designated ATCC9-Mtb [in Table 1] SEQ ID NO:1 or its complement, wherein the  
5 segment includes a highlighted nucleotide position [shown in Table 1] designated as any of the  
6 SEQ ID NOS: 1-181.

1 12. (Twice Amended) The sequence-specific polynucleotide of claim 9 that  
2 is a probe.

1 13. (Twice Amended) The sequence-specific polynucleotide of claim 12,  
2 wherein a central position of the probe aligns with a highlighted nucleotide position [shown in  
3 Tables 13] designated as any of the SEQ ID NOS: 1-181.

1 14. (Once Amended) The sequence-specific polynucleotide of claim 9 that  
2 is a primer.

1 15. (Twice Amended) The sequence-specific polynucleotide of claim 14,  
2 wherein the 3' end of the primer aligns with a highlighted nucleotide position [shown in Table  
3 13] designated as any of the SEQ ID NOS: 1-181.

1 16. (Once Amended) The sequence-specific polynucleotide of claim 8 that  
2 is between 10 and 50 bases long.

1 17. (Twice Amended) A computer-readable storage medium for storing  
2 data for access by an application program being executed on a data processing system,  
3 comprising:

4 a data structure stored in the computer-readable storage medium, the data  
5 structure including information resident in a database used by the application program and  
6 including:

7 a plurality of records, each record comprising information identifying a  
8 polymorphism or sequence [shown in Table 1] designated as any of the SEQ ID NOS: 1-181.

1 18. (Once Amended) The computer-readable storage medium of claim 17,  
2 wherein each record has a field identifying a base occupying a polymorphic site and a field  
3 identifying location of the polymorphic site.

1 19. (Twice Amended) The computer-readable storage medium of claim 17,  
2 wherein each record records a contiguous segment of at least 50 bases from an rpoB sequence  
3 [shown in Table 1] designated as any of the SEQ ID NOS: 1-181.

1 20. (Twice Amended) The computer-readable storage medium of claim 19,  
2 comprising at least ten records each recording a contiguous segment of at least 50 bases from  
3 at least ten rpoB sequences [shown in Table 1] designated as SEQ ID NOS: 1-181.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§  
1.821 to 1.825. This amendment contains no new matter.

The Examiner has asserted that the claims refer to sequences that are not  
identified by SEQ ID NOS. Applicants amends the claims to remove references to Table 1,  
inserting therefor references to SEQ ID NOS:1-181. No new matter is introduced by these  
amendments, and support for the amendments is found in Table 1 itself, which contains SEQ  
ID NOS:1-181.